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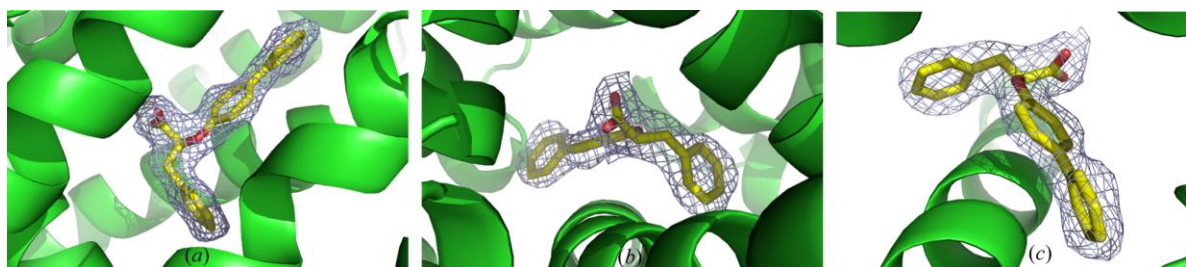
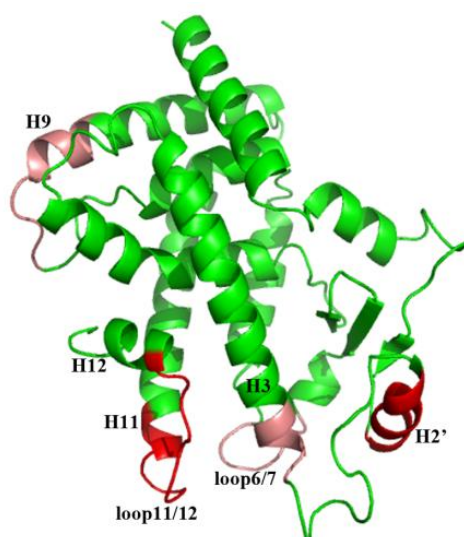
Supporting information for article:

Structural basis of the transactivation deficiency of human PPAR γ F360L mutant associated with familial partial lipodystrophy

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Table S1 List of oligonucleotides used for site-directed mutagenesis.

F360L Fw-CGAAAGCCTCTGGGTGACTTTA
F360L Rev-TAAAGTCACCCAGAGGCTTTCG
R357A Fw-GGAGTTTCTAAAGAGCCTGGCAAAGCCTTTTGGTGACTTTAT
R357A Rev-ATAAAGTCACCAAAGGCTTTGCCAGGCTCTTTAGAAACTCC

**Figure S1.** Omit $2F_o - F_c$ electron-density maps calculated around (a) molecule A and (b) molecule B of the ligand LT175 ($P2_12_12$), and (c) molecule A of LT175 ($I222$). All the maps are contoured at the 1σ level.**Figure S2.** Regions of the PPAR γ R357A LBD complexed with rosiglitazone with markedly (red color) and less markedly (pink color) higher B-factors with respect to the corresponding WT crystal structure with the same ligand. The variation of B-factors regarding helix 8 is less relevant because in the WT structure this helix is affected by crystal packing interactions.

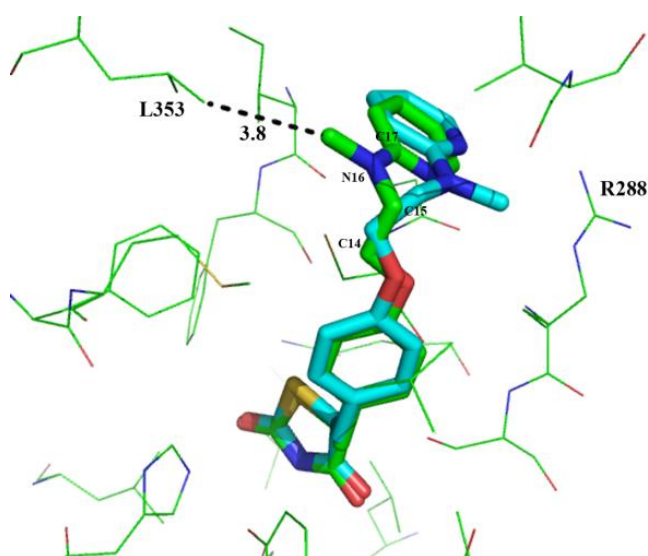


Figure S3. Superposition of molecules A of rosiglitazone in R357A (green color) and WT (cyan color), respectively.

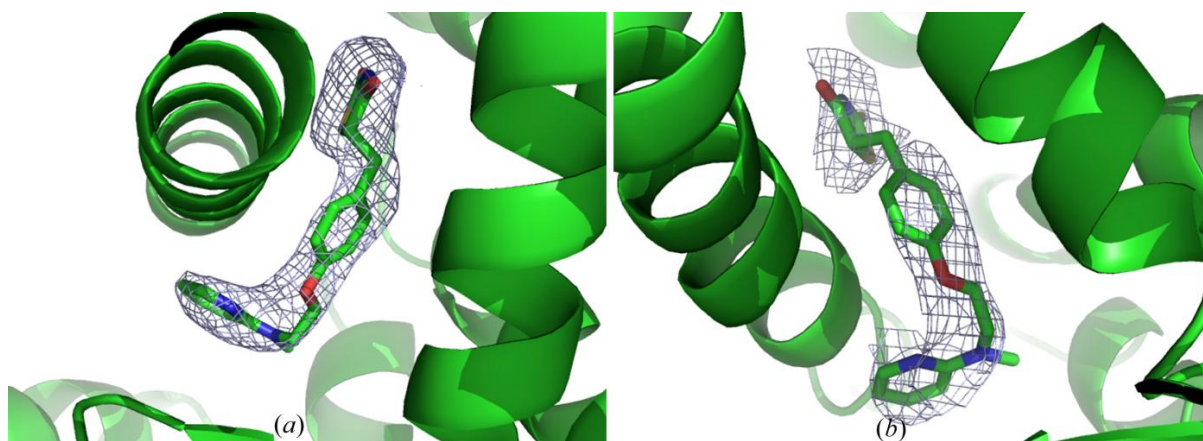


Figure S4. Omit $2F_o - F_c$ electron-density maps calculated around (a) molecule A and (b) molecule B of the ligand rosiglitazone. All the maps are contoured at the 1σ level.

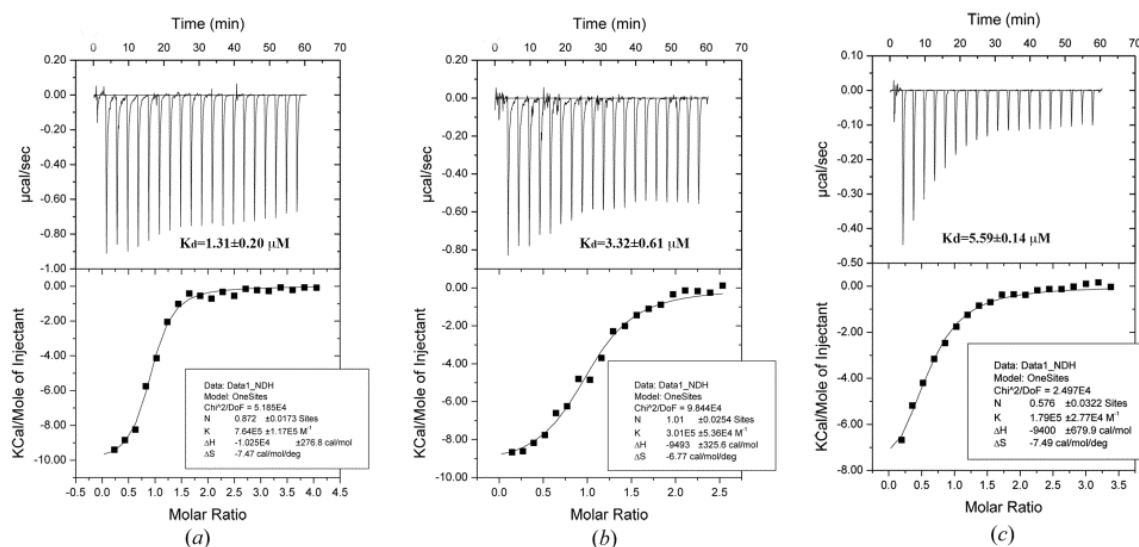


Figure S5. ITC experiments: binding of SRC-1 to (a) WT, (b) F360L and (c) R357A after equilibration with LT175.

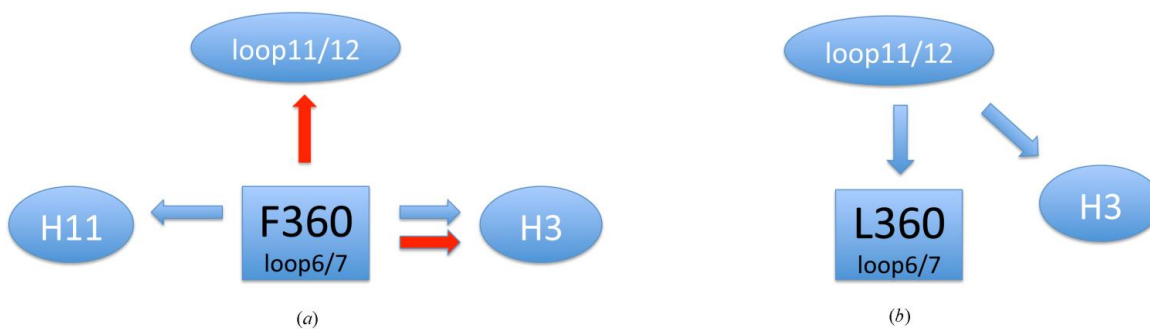


Figure S6. Blocks diagram of the interactions between H3, H11, loop 6/7 and loop 11/12 in (a) WT PPAR γ and (b) F360L mutant. Light blue arrows indicate vdW interactions, red arrows a salt-bridge.